SEQUENCE LISTING

<110> Kindsvogel, Wayne R.
      Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOKINE RECEPTORS

<130> 00-56

<150> US 60/223,827
<151> 2000-08-08

<150> US 60/250,876
<151> 2000-12-01

<160> 35

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<212> DNA
<213> Homo sapien

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<222> (34)...(1755)

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                                      1               5

ttg act gtg gga tcc ctg gct gct cac gcc cct gag gac ccc tcg gat     102
Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp
         10                  15                  20

ctg ctc cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg     150
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu
     25                  30                  35

acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc     198
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Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile
40   45   50   55

gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt   246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys
                60   65   70

cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac   294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn
              75   80   85

ctc acg gag ctc tac tat gcc agg gtc acc gct gtc agt gcg gga ggc   342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly
            90   95   100

cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act   390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr
        105   110   115

acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att   438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile
120   125   130   135

cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc   486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly
              140   145   150

cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta   534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu
            155   160   165

gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag   582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln
        170   175   180

aga gaa tat gag ttc ttc ggc ctg acc cct gac aca gag ttc ctt ggc   630
Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly
      185   190   195

acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac   678
Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr
200   205   210   215

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atg tgc cga gtg aag aca ctg cca gac cgg aca tgg acc tac tcc ttc    726
Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe
                220                 225                 230

tcc gga gcc ttc ctg ttc tcc atg ggc ttc ctc gtc gca gta ctc tgc    774
Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys
                235                 240                 245

tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc    822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser
                250                 255                 260

ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag    870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln
        265                 270                 275

gag cac gtc ctg atc cct gtc ttt gac ctc agc ggc ccc agc agt ctg    918
Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu
280                 285                 290                 295

gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag    966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu
                300                 305                 310

ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta   1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu
                315                 320                 325

ggg cag cca gac atc tcc atc ctc cag ccc tcc aac gtg cca cct ccc   1062
Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro
                330                 335                 340

cag atc ctc tcc cca ctg tcc tat gcc cca aac gct gcc cct gag gtc   1110
Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val
        345                 350                 355

ggg ccc cca tcc tat gca cct cag gtg acc ccc gaa gct caa ttc cca   1158
Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro
360                 365                 370                 375

ttc tac gcc cca cag gcc atc tct aag gtc cag cct tcc tcc tat gcc   1206
Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala
                380                 385                 390
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cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg    1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met
            395                 400                 405

gaa ggt tct ggc aaa gac tcc ccc act ggg aca ctt tct agt cct aaa    1302
Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys
            410                 415                 420

cac ctt agg cct aaa ggt cag ctt cag aaa gag cca cca gct gga agc    1350
His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser
        425                 430                 435

tgc atg tta ggt ggc ctt tct ctg cag gag gtg acc tcc ttg gct atg    1398
Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met
440                 445                 450                 455

gag gaa tcc caa gaa gca aaa tca ttg cac cag ccc ctg ggg att tgc    1446
Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys
                460                 465                 470

aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg    1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly
            475                 480                 485

aca cca cag tac cta aag ggc cag ctc ccc ctc ctc tcc tca gtc cag    1542
Thr Pro Gln Tyr Leu Lys Gly Gln Leu Pro Leu Leu Ser Ser Val Gln
            490                 495                 500

atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca    1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro
        505                 510                 515

tgt tcc ccc tcg gac caa ggt cca agt ccc tgg ggc ctg ctg gag tcc    1638
Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser
520                 525                 530                 535

ctt gtg tgt ccc aag gat gaa gcc aag agc cca gcc cct gag acc tca    1686
Leu Val Cys Pro Lys Asp Glu Ala Lys Ser Pro Ala Pro Glu Thr Ser
            540                 545                 550

gac ctg gag cag ccc aca gaa ctg gat tct ctt ttc aga ggc ctg gcc    1734
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Asp Leu Glu Gln Pro Thr Glu Leu Asp Ser Leu Phe Arg Gly Leu Ala
            555                 560                 565

ctg act gtg cag tgg gag tcc tgaggggaat gggaaaggct tggtgcttcc      1785
Leu Thr Val Gln Trp Glu Ser
        570

tccctgtccc tacccagtgt cacatccttg gctgtcaatc ccatgcctgc ccatgccaca      1845
cactctgcga tctggcctca gacgggtgcc cttgagagaa gcagagggag tggcatgcag      1905
ggcccctgcc atgggtgcgc tcctcaccgg aacaaagcag catgataagg actgcagcgg      1965
gggagctctg gggagcagct tgtgtagaca agcgcgtgct cgctgagccc tgcaaggcag      2025
aaatgacagt gcaaggagga aatgcaggga aactcccgag gtccagagcc ccacctccta      2085
acaccatgga ttcaaagtgc tcagggaatt tgcctctcct tgccccattc ctggccagtt      2145
tcacaatcta gctcgacaga gcatgaggcc cctgcctctt ctgtcattgt tcaaaggtgg      2205
gaagagagcc tggaaaagaa ccaggcctgg aaaagaacca gaaggaggct gggcagaacc      2265
agaacaacct gcacttctgc caaggccagg gccagcagga cggcaggact ctagggaggg      2325
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tttctgcagg caggagtttc agaccctatc ctgagaatgg ggtttgaaag gaaggtgagg      2505
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ataacaccta cctcatggag ttgtggtgaa gatgaaatga agtcatgtct ttaaagtgct      2745
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        <213> Homo sapien

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Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80
```

Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85   90   95
Thr Ala Val Ser Ala Gly Gly Arg Ser Thr Lys Met Thr Asp Arg
                100   105   110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
                115   120   125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
        130   135   140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145   150   155   160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165   170   175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
                180   185   190
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
                195   200   205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
        210   215   220
Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly
225   230   235   240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys
                245   250   255
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe
                260   265   270
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp
        275   280   285
Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile
        290   295   300
Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser
305   310   315   320
Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln
                325   330   335
Pro Ser Asn Val Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala
                340   345   350
Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val
        355   360   365
Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys
        370   375   380
Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro
385   390   395   400
Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr
                405   410   415

```
Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln
        420                 425                 430
Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln
        435                 440                 445
Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu
    450                 455                 460
His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val
465                 470                 475                 480
Leu His Ser Gly Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu
                485                 490                 495
Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro
        500                 505                 510
Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser
        515                 520                 525
Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys
    530                 535                 540
Ser Pro Ala Pro Glu Gln Thr Ser Asp Leu Glu Gln Pro Thr Glu Leu Asp
545                 550                 555                 560
Ser Leu Phe Arg Gly Leu Ala Leu Thr Val Gln Trp Glu Ser
                565                 570
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        <212> PRT
        <213> Homo sapiens

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Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro
            20                  25                  30
Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp
            35                  40                  45
Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu
    50                  55                  60
Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr
65                  70                  75                  80
Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe
            85                  90                  95
Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile
            100                 105                 110
```

Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro
    115   120   125

Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His
    130   135   140

Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met
145   150   155   160

His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro
        165   170   175

Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala
        180   185   190

Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg
        195   200   205

Thr Trp Thr
    210

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    <212> PRT
    <213> Artificial Sequence

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    <223> Glu-Glu peptide tag

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Glu Tyr Met Pro Met Glu
  1   5

    <210> 5
    <211> 8
    <212> PRT
    <213> Artificial Sequence

    <220>
    <223> Flag-tag peptide

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Asp Tyr Lys Asp Asp Asp Asp Lys
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    <210> 6
    <211> 699
    <212> DNA

<213> Homo sapiens

<400> 6

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gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag    60
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg   120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc   180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag   240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat   300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc   360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg   420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc   480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   540
cccgtgctgg actccgacgg ctccttcttc tctctacagca agctcaccgt ggacaagagc   600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac   660
tacacgcaga agagcctctc cctgtctccg ggtaaataa                          699
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<213> homo sapiens

<220>
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<222> (21)...(557)

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                         1               5                      10


ctt atg ggg acc ctg gcc acc agc tgc ctc ctt ctc ttg gcc ctc ttg   101
Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
             15                  20                  25


gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac   149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
         30                  35                  40


aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg   197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
     45                  50                  55


gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att   245
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Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
 60                  65                  70                      75

ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg      293
Gly Glu Lys Leu Phe His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu
                 80                  85                  90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa      341
Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln
                 95                 100                 105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc      389
Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala
             110                 115                 120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg      437
Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu
     125                 130                 135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt      485
His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu
140                 145                 150                 155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt      533
Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe
                 160                 165                 170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac      587
Met Ser Leu Arg Asn Ala Cys Ile
                 175

taaccccctt tccctgctag aaataacaat tagatgcccc aaagcgattt tttttaacca      647
aaaggaagat gggaagccaa actccatcat gatgggtgga ttccaaatga acccctgcgt      707
tagttacaaa ggaaaccaat gccacttttg tttataagac cagaaggtag actttctaag      767
catagatatt tattgataac atttcattgt aactggtgtt ctatacacag aaaacaattt      827
attttttaaa taattgtctt tttccataaa aaagattact ttccattcct ttaggggaaa      887
aaacccctaa atagcttcat gtttccataa tcagtacttt atatttataa atgtatttat      947
tattattata agactgcatt ttatttatat cattttatta atatggattt atttatagaa     1007
acatcattcg atattgctac ttgagtgtaa ggctaatatt gatatttatg acaataatta     1067
tagagctata acatgtttat ttgacctcaa taaacacttg gatatcccta                1116

        <210> 8
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<212> PRT
<213> homo sapiens

<400> 8

Met Ala Ala Leu Gln Lys Ser Val Ser Ser Phe Leu Met Gly Thr Leu
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Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu Val Gln Gly Gly Ala
            20   25   30
Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln
        35   40   45
Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser
    50   55   60
Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe
65   70   75   80
His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu
                85   90   95
Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln Ser Asp Arg Phe Gln
            100   105   110
Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg
        115   120   125
Leu Ser Glu Thr Cys His Ile Glu Gly Asp Asp Leu His Ile Gln Arg Asn
    130   135   140
Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu
145   150   155   160
Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe Met Ser Leu Arg Asn
                165   170   175
Ala Cys Ile

<210> 9
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<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide prime ZC28590

<400> 9
ttgggtacct ctgcaatggc cgccctgcag aaatct   36

<210> 10
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<212> DNA
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<220>
<223> Oligonucleotide prime ZC28580

<400> 10
ttgggatcca atgcaggcat ttctcagaga cat   33

<210> 11
<211> 18
<212> DNA
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<220>
<223> Oligonucleotide prime ZC14666

<400> 11
agccaccaag atgactga   18

<210> 12
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<212> DNA
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<220>
<223> Oligonucleotide prime ZC14742

<400> 12
tgcatttggt aggtgcggtt ga   22

<210> 13
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> His tag

<400> 13
His His His His His His
1   5

<210> 14
<211> 63

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<212> DNA
<213> Artificial Sequence

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<223> Oligonucleotide primer ZC29239

<400> 14
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gaggccggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca   60
tgc   63

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<210> 15
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<212> DNA
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<223> Oligonucleotide primer ZC29232

<400> 15
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cgactgactc gagtcagtga tggtgatggt gatggccacc tgatccttta cccggagaca   60
gggag   65

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<223> Oligonucleotide primer ZC39319

<400> 16
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atcggaattc gcagaagcca tggcgtggag ccttggg   37

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<210> 17
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<223> Oligonucleotide primer ZC39325

<400> 17
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cagtggatcc ggaggggacc gtttcgtc   28

<210> 18
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<213> Homo sapiens

<220>
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<222> (1)...(660)

<400> 18

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Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1               5                   10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt      96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg     144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat     192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
    50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc     240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag     288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att     336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
                100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat     384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
            115                 120                 125
```

```
atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act    432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa    480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160

aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag    528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175

gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga    576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
                180                 185                 190

ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc    624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
                195                 200                 205

tgt gag caa aca acc cat gac gaa acg gtc ccc tcc                    660
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
    210                 215                 220

        <210> 19
        <211> 220
        <212> PRT
        <213> Homo sapiens

        <400> 19
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1               5                   10                  15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
                20                  25                  30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
            35                  40                  45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
        50                  55                  60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95
```

His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
       100   105   110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
       115   120   125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
       130   135   140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145   150   155   160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
             165   170   175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180   185   190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
       195   200   205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser
   210   215   220

```
<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC38931

<400> 20
```
acaaagccgc gggaggag   18

```
<210> 21
<211> 82
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39042

<400> 21
```
ctgactcgag tcagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca   60
gtttacccgg agacagggag ag   82

```
<210> 22
<211> 1428
```

```
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)...(1428)

<223> CRF2-4 extracellular cytokine binding domain fused
     to IgGg1 with a 6-HIS tag

<400> 22
atg gcg tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca      48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1               5                   10                  15

gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt      96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
            20                  25                  30

aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg     144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45

aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat     192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
        50                  55                  60

aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc     240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80

aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag     288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95

cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att     336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
                100                 105                 110

att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat     384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125
```

```
atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act       432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
    130                 135                 140
```

```
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa       480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160
```

```
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag       528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
            165                 170                 175
```

```
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga       576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
            180                 185                 190
```

```
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc       624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
            195                 200                 205
```

```
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tcg       672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
    210                 215                 220
```

```
ggt tcg ggt tcg gag ccc aga tca tca gac aaa act cac aca tgc cca       720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
225                 230                 235                 240
```

```
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc       768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
                245                 250                 255
```

```
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc       816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                260                 265                 270
```

```
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc       864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
                275                 280                 285
```

```
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg       912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
    290                 295                 300
```

```
cgg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc    960
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305             310             315                 320

gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc    1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                325             330             335

tcc aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc    1056
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
            340             345             350

aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg    1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            355             360             365

gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc    1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        370             375             380

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg    1200
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385             390             395                 400

gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc    1248
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                405             410             415

ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag    1296
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            420             425             430

ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac    1344
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            435             440             445

tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt    1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
        450             455             460

ggt tcc gga tca ggt ggc cat cac cat cac cat cac                    1428
Gly Ser Gly Ser Gly Gly His His His His His His
```

```
Gly Ser Gly Ser Gly Gly His His His His His His
465                 470                 475
```

```
        <210> 23
        <211> 476
        <212> PRT
        <213> Homo sapiens


        <400> 23
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser
1               5                   10                  15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val
        20                  25                  30
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly
        35                  40                  45
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp
        50                  55                  60
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser
65                  70                  75                  80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu
                85                  90                  95
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile
                100                 105                 110
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His
        115                 120                 125
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr
        130                 135                 140
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys
145                 150                 155                 160
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu
                165                 170                 175
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg
                180                 185                 190
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val
        195                 200                 205
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser
        210                 215                 220
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro
225                 230                 235                 240
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe
                245                 250                 255
```

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
                260   265   270

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
            275   280   285

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
        290   295   300

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
305   310   315   320

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
                325   330   335

Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala
            340   345   350

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
            355   360   365

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
        370   375   380

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
385   390   395   400

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
                405   410   415

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
            420   425   430

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
            435   440   445

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg
        450   455   460

Gly Ser Gly Ser Gly Gly His His His His His
465   470   475

        <210> 24
        <211> 63
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> Oligonucleotide primer ZC29328

        <400> 24
tcagagggat ccggttcggg ttcgggttcg gagcccagat catcagacaa aactcacaca   60
tgc   63

        <210> 25

<211> 65
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC29231

<400> 25
cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca   60
gggag   65

<210> 26
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39335

<400> 26
atcggaattc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc   60
tgctcacgcc   70

<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC28981

<400> 27
tttgggctcc ctgagctctg gtggaa   26

<210> 28
<211> 80
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC39043

<400> 28

```
ctgactcgag ctactccata ggcatatact cgccacctga tccggaacca cgcggaacca      60
gtttacccgg agacagggag                                                   80
```

        <210> 29
        <211> 1452
        <212> DNA
        <213> Artificial Sequence

        <220>
        <223> hzcytor11 extracellular cytokine binding domain
              fused to IgGg1 with a Glu-Glu tag

        <221> CDS
        <222> (1)...(1452)

        <400> 29

```
atg agg acg ctg ctg acc atc ttg act gtg gga tcc ctg gct gct cac      48
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
1               5                   10                  15

gcc cct gag gac ccc tcg gat ctg ctc cag cac gtg aaa ttc cag tcc      96
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
            20                  25                  30

agc aac ttt gaa aac atc ctg acg tgg gac agc ggg cca gag ggc acc     144
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45

cca gac acg gtc tac agc atc gag tat aag acg tac gga gag agg gac     192
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60

tgg gtg gca aag aag ggc tgt cag cgg atc acc cgg aag tcc tgc aac     240
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80

ctg acg gtg gag acg ggc aac ctc acg gag ctc tac tat gcc agg gtc     288
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95

acc gct gtc agt gcg gga ggc cgg tca gcc acc aag atg act gac agg     336
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110
```

```
ttc agc tct ctg cag cac act acc ctc aag cca cct gat gtg acc tgt        384
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
            115                     120                 125

atc tcc aaa gtg aga tcg att cag atg att gtt cat cct acc ccc acg        432
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
        130                     135                 140

cca atc cgt gca ggc gat ggc cac cgg cta acc ctg gaa gac atc ttc        480
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                     150                 155                 160

cat gac ctg ttc tac cac tta gag ctc cag gtc aac cgc acc tac caa        528
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                    165                 170                 175

atg cac ctt gga ggg aag cag aga gaa tat gag ttc ttc ggc ctg acc        576
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
                180                 185                 190

cct gac aca gag ttc ctt ggc acc atc atg att tgc gtt ccc acc tgg        624
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
            195                 200                 205

gcc aag gag agt gcc ccc tac atg tgc cga gtg aag aca ctg cca gac        672
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
        210                 215                 220

cgg aca tgg acc gga tcc ggt tcg ggt tcg ggt tcg gag ccc aga tca        720
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
225                 230                 235                 240

tca gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag        768
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
                245                 250                 255

ggg gca ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc        816
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
                260                 265                 270

atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc        864
```

```
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
```

```
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag    912
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    290                 295                 300
```

```
gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg    960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
```

```
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat    1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
```

```
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc    1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
            340                 345                 350
```

```
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag    1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
            355                 360                 365
```

```
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc    1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    370                 375                 380
```

```
agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac atc gcc gtg    1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
```

```
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct    1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
```

```
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc    1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
```

```
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg    1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
```

```
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg     1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    450                 455                 460

tct ccg ggt aaa ctg gtt ccg cgt ggt tcc gga tca ggt ggc gag tat     1440
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
465                 470                 475                 480

atg cct atg gag                                                      1452
Met Pro Met Glu
```

<210> 30
<211> 484
<212> PRT
<213> Artificial Sequence

<400> 30

```
Met Arg Thr Leu Leu Thr Ile Leu Thr Val Gly Ser Leu Ala Ala His
1               5                   10                  15
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser
        20                  25                  30
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr
        35                  40                  45
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp
    50                  55                  60
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn
65                  70                  75                  80
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val
                85                  90                  95
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg
            100                 105                 110
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys
        115                 120                 125
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr
        130                 135                 140
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe
145                 150                 155                 160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln
                165                 170                 175
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr
            180                 185                 190
```

```
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp
        195                 200                 205
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp
        210                 215                 220
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser
225                 230                 235                 240
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu
                245                 250                 255
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            260                 265                 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        275                 280                 285
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
        290                 295                 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
305                 310                 315                 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                325                 330                 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser
            340                 345                 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        355                 360                 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
        370                 375                 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
385                 390                 395                 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                405                 410                 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            420                 425                 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        435                 440                 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
        450                 455                 460
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr
465                 470                 475                 480
Met Pro Met Glu
```

        <210> 31
        <211> 22
        <212> DNA
        <213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC37693

<400> 31
ccccagacac ggtctacagc at   22

<210> 32
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide primer ZC37449

<400> 32
gggtcaggcc gaagaactca tat   23

<210> 33
<211> 199
<212> PRT
<213> Homo sapiens

<400> 33
Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val Asn Phe Lys
1   5   10   15
Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly Asn Leu Thr
            20   25   30
Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met
        35   40   45
Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly
    50   55   60
Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp
65   70   75   80
Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro
                85   90   95
Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe
            100   105   110
Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn
        115   120   125
Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr
    130   135   140

Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg
145   150   155   160
Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu
                    165   170   175
Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln
                180   185   190
Thr Thr His Asp Glu Thr Val
            195

        <210> 34
        <211> 211
        <212> PRT
        <213> Homo sapiens

        <400> 34
Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe
1   5   10   15
Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn
                    20   25   30
Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile
            35   40   45
Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp
        50   55   60
Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala
65   70   75   80
Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr
                    85   90   95
Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val
                100   105   110
Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro
            115   120   125
Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser
        130   135   140
His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe
145   150   155   160
Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr
                    165   170   175
Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala
                180   185   190
Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu
            195   200   205

Thr Arg Gln
    210

        <210> 35
        <211> 201
        <212> PRT
        <213> Homo sapiens

        <400> 35
Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser
1   5   10   15
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly
            20   25   30
Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu
            35   40   45
Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu
        50   55   60
Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr
65   70   75   80
Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser
                85   90   95
Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro
                100   105   110
Gly Met Glu Ile Thr Lys Asp Gly Phe His Leu Val Ile Glu Leu Glu
            115   120   125
Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Arg Arg Glu
        130   135   140
Pro Gly Ala Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro
145   150   155   160
Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala
                165   170   175
Gln Thr Phe Val Lys Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr
                180   185   190
Glu Cys Val Glu Val Gln Gly Glu Ala
        195   200